



SYR-HDAC-5005-C2 sub seq list 2.ST25  
SEQUENCE LISTING

<110> Syrrx, Inc.

<120> HISTONE DEACETYLASE INHIBITORS

<130> SYR-HDAC-5005-C2

<140> US 10/803,580

<141> 2004-03-17

<150> US 60/455,437

<151> 2003-03-17

<150> US 60/531,203

<151> 2003-12-19

<160> 8

<170> PatentIn version 3.2

<210> 1

<211> 513

<212> PRT

<213> Artificial

<220>

<223> Residues 1-482 of HDAC1 with a "MSYYHHHHHDYDIPTTENLYFQGAMEPGGS"  
tag at the N-terminus

<400> 1

Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr  
1 5 10 15

Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Glu Pro Gly Gly Ser Met  
20 25 30

Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp Gly  
35 40 45

Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His  
50 55 60

Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr Arg  
65 70 75 80

Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met Thr  
85 90 95

Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg Pro  
100 105 110

Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val Gly  
115 120 125

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Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu Ser  
 130 135 140  
 Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln Thr  
 145 150 155 160  
 Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys Ser  
 165 170 175  
 Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile Leu  
 180 185 190  
 Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp Ile  
 195 200 205  
 His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Val  
 210 215 220  
 Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr Gly  
 225 230 235 240  
 Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val Asn  
 245 250 255  
 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe  
 260 265 270  
 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val  
 275 280 285  
 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys  
 290 295 300  
 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys  
 305 310 315 320  
 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile  
 325 330 335  
 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp  
 340 345 350  
 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe  
 355 360 365  
 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln  
 370 375 380

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Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn  
385 390 395 400

Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro  
405 410 415

Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro  
420 425 430

Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu  
435 440 445

Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn  
450 455 460

Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys  
465 470 475 480

Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr  
485 490 495

Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys Leu  
500 505 510

Ala

<210> 2  
<211> 1542  
<212> DNA  
<213> Artificial

<220>  
<223> DNA sequence encoding residues 1-482 of HDAC1 with a  
"MSYYHHHHHDYDIPTTENLYFQGAMEPGGS" tag at the N-terminus

<400> 2  
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tattttcagg gcgccatgga acccggggga tccatggcgc agacgcaggg caccggagg 120  
aaagtctgtt actactacga cggggatgtt ggaaattact attatggaca aggccacca 180  
atgaagcctc accgaatccg catgactcat aatttgctgc tcaactatgg tctctaccga 240  
aaaatggaaa tctatcgccc tcacaaagcc aatgctgagg agatgaccaa gtaccacagc 300  
gatgactaca ttaaattctt gcgctccatc cgtccagata acatgtcgga gtacagcaag 360  
cagatgcaga gattcaacgt tggtgaggac tgtccagtat tcgatggcct gtttgagttc 420  
tgtcagttgt ctactggtgg ttctgtggca agtgctgtga aacttaataa gcagcagacg 480

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gacatcgctg tgaattgggc tgggggcctg caccatgcaa agaagtccga ggcattctggc 540  
 ttctgttacg tcaatgatat cgtcttggcc atcctggaac tgctaaagta tcaccagagg 600  
 gtgctgtaca ttgacattga tattcaccat ggtgacggcg tggaagaggc cttctacacc 660  
 acggaccggg tcatgactgt gtcctttcat aagtatggag agtacttccc aggaactggg 720  
 gacctacggg atatcggggc tggcaaaggc aagtattatg ctgttaacta cccgctccga 780  
 gacgggattg atgacgagtc ctatgaggcc attttcaagc cggtcatgtc caaagtaatg 840  
 gagatgttcc agcctagtgc ggtggtctta cagtgtggct cagactccct atctggggat 900  
 cggttagggt gcttcaatct aactatcaaa ggacacgcca agtgtgtgga atttgtcaag 960  
 agctttaacc tgcctatgct gatgctggga ggcgggtggt acaccattcg taacgttgcc 1020  
 cggtgctgga catatgagac agctgtggcc ctggatacgg agatccctaa tgagcttcca 1080  
 tacaatgact actttgaata ctttggacca gatttcaagc tccacatcag tccttccaat 1140  
 atgactaacc agaacacgaa tgagtacctg gagaagatca aacagcgact gtttgagaac 1200  
 cttagaatgc tgccgcacgc acctggggtc caaatgcagg cgattcctga ggacgccatc 1260  
 cctgaggaga gtggcgatga ggacgaagac gaccctgaca agcgcatctc gatctgctcc 1320  
 tctgacaaac gaattgcctg tgaggaagag ttctccgatt ctgaagagga gggagagggg 1380  
 ggccgcaaga actcttccaa cttcaaaaaa gccaagagag tcaaaacaga ggatgaaaaa 1440  
 gagaaagacc cagaggagaa gaaagaagtc accgaagagg agaaaaccaa ggaggagaag 1500  
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<210> 3  
 <211> 498  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Residues 1-488 of HDAC2 with a "GHHHHH" tag at the C-terminus  
 and a "MGS" tag at the N-terminus

<400> 3

Met Gly Ser Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Val Cys  
 1 5 10 15

Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His  
 20 25 30

Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn  
 35 40 45

Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr  
 50 55 60

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Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu  
65 70 75 80

Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln  
85 90 95

Arg Phe Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu  
100 105 110

Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu  
115 120 125

Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His  
130 135 140

His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile  
145 150 155 160

Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr  
165 170 175

Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr  
180 185 190

Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr  
195 200 205

Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys  
210 215 220

Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu Ser  
225 230 235 240

Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr  
245 250 255

Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly  
260 265 270

Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys  
275 280 285

Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly  
290 295 300

Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr  
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 305 310 315 320

Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp  
 325 330 335

Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser  
 340 345 350

Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln  
 355 360 365

Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln  
 370 375 380

Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu  
 385 390 395 400

Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys  
 405 410 415

Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu  
 420 425 430

Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala  
 435 440 445

Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val  
 450 455 460

Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr  
 465 470 475 480

Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro Gly His His His His  
 485 490 495

His His

<210> 4  
 <211> 1497  
 <212> DNA  
 <213> Artificial

<220>  
 <223> DNA sequence encoding residues 1-488 of HDAC2 with a "GHHHHHH" tag at the C-terminus and a "MGS" tag at the N-terminus

<400> 4  
 atgggatcca tggcgtacag tcaaggaggc ggcaaaaaaa aagtctgcta ctactacgac 60

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ggtgatattg gaaattatta ttatggacag ggtcatccca tgaagcctca tagaatccgc	120
atgaccata acttgctgtt aaattatggc ttatacagaa aaatggaaat atataggccc	180
cataaagcca ctgccgaaga aatgacaaaa tatcacagtg atgagtatat caaatttcta	240
cgggtcaataa gaccagataa catgtctgag tatagtaagc agatgcagag atttaatggt	300
ggagaagatt gtccagtgtt tgatggactc tttgagtttt gtcagctctc aactggcggg	360
tcagttgctg gagctgtgaa gttaaaccga caacagactg atatggctgt taattgggct	420
ggaggattac atcatgctaa gaaatcagaa gcatcaggat tctgttacgt taatgatatt	480
gtgcttgcca tccttgaatt actaaagtat catcagagag tcttatatat tgatatagat	540
attcatcatg gtgatgggtg tgaagaagct ttttatacaa cagatcgtgt aatgacggta	600
tcattccata aatatgggga atactttcct ggcacaggag acttgaggga tattggtgct	660
ggaaaaggca aatactatgc tgtcaatttt ccaatgagag atggtataga tgatgagtca	720
tatgggcaga tatttaagcc tattatctca aagggtgatg agatgtatca acctagtgt	780
gtggtattac agtgtggtgc agactcatta tctggtgata gactgggttg tttcaatcta	840
acagtcaaag gtcattgctaa atgtgtagaa gttgtaaaaa cttttaactt accattactg	900
atgcttggag gaggtggcta cacaatccgt aatgttgctc gatgttggac atatgagact	960
gcagttgccc ttgattgtga gattcccaat gagttgccat ataatgatta ctttgagtat	1020
tttgaccag acttcaaact gcatattagt ccttcaaaca tgacaaacca gaacactcca	1080
gaatatatgg aaaagataaa acagcgtttg tttgaaaatt tgcgcattgt acctcatgca	1140
cctggtgtcc agatgcaagc tattccagaa gatgctgttc atgaagacag tggagatgaa	1200
gatggagaag atccagacaa gagaatttct attcgagcat cagacaagcg gatagcttgt	1260
gatgaagaat tctcagattc tgaggatgaa ggagaaggag gtcgaagaaa tgtggctgat	1320
cataagaaag gagcaaagaa agctagaatt gaagaagata agaaagaaac agaggacaaa	1380
aaaacagacg ttaaggaaga agataaatcc aaggacaaca gtggtgaaaa aacagatacc	1440
aaaggaacca aatcagaaca gctcagcaac cccgggcatc accatcacca tcaactaa	1497

<210> 5  
 <211> 782  
 <212> PRT  
 <213> Artificial

<220>  
 <223> Residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus  
 and a "MP" tag at the N-terminus

<400> 5

Met	Pro	Gly	Met	Asp	Leu	Asn	Leu	Glu	Ala	Glu	Ala	Leu	Ala	Gly	Thr
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Gly Leu Val Leu Asp Glu Gln Leu Asn Glu Phe His Cys Leu Trp Asp  
20 25 30

Asp Ser Phe Pro Glu Gly Pro Glu Arg Leu His Ala Ile Lys Glu Gln  
35 40 45

Leu Ile Gln Glu Gly Leu Leu Asp Arg Cys Val Ser Phe Gln Ala Arg  
50 55 60

Phe Ala Glu Lys Glu Glu Leu Met Leu Val His Ser Leu Glu Tyr Ile  
65 70 75 80

Asp Leu Met Glu Thr Thr Gln Tyr Met Asn Glu Gly Glu Leu Arg Val  
85 90 95

Leu Ala Asp Thr Tyr Asp Ser Val Tyr Leu His Pro Asn Ser Tyr Ser  
100 105 110

Cys Ala Cys Leu Ala Ser Gly Ser Val Leu Arg Leu Val Asp Ala Val  
115 120 125

Leu Gly Ala Glu Ile Arg Asn Gly Met Ala Ile Ile Arg Pro Pro Gly  
130 135 140

His His Ala Gln His Ser Leu Met Asp Gly Tyr Cys Met Phe Asn His  
145 150 155 160

Val Ala Val Ala Ala Arg Tyr Ala Gln Gln Lys His Arg Ile Arg Arg  
165 170 175

Val Leu Ile Val Asp Trp Asp Val His His Gly Gln Gly Thr Gln Phe  
180 185 190

Thr Phe Asp Gln Asp Pro Ser Val Leu Tyr Phe Ser Ile His Arg Tyr  
195 200 205

Glu Gln Gly Arg Phe Trp Pro His Leu Lys Ala Ser Asn Trp Ser Thr  
210 215 220

Thr Gly Phe Gly Gln Gly Gln Gly Tyr Thr Ile Asn Val Pro Trp Asn  
225 230 235 240

Gln Val Gly Met Arg Asp Ala Asp Tyr Ile Ala Ala Phe Leu His Val  
245 250 255

Leu Leu Pro Val Ala Leu Glu Phe Gln Pro Gln Leu Val Leu Val Ala  
260 265 270



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Ala Gly Phe Asp Ala Leu Gln Gly Asp Pro Lys Gly Glu Met Ala Ala  
275 280 285

Thr Pro Ala Gly Phe Ala Gln Leu Thr His Leu Leu Met Gly Leu Ala  
290 295 300

Gly Gly Lys Leu Ile Leu Ser Leu Glu Gly Gly Tyr Asn Leu Arg Ala  
305 310 315 320

Leu Ala Glu Gly Val Ser Ala Ser Leu His Thr Leu Leu Gly Asp Pro  
325 330 335

Cys Pro Met Leu Glu Ser Pro Gly Ala Pro Cys Arg Ser Ala Gln Ala  
340 345 350

Ser Val Ser Cys Ala Leu Glu Ala Leu Glu Pro Phe Trp Glu Val Leu  
355 360 365

Val Arg Ser Thr Glu Thr Val Glu Arg Asp Asn Met Glu Glu Asp Asn  
370 375 380

Val Glu Glu Ser Glu Glu Glu Gly Pro Trp Glu Pro Pro Val Leu Pro  
385 390 395 400

Ile Leu Thr Trp Pro Val Leu Gln Ser Arg Thr Gly Leu Val Tyr Asp  
405 410 415

Gln Asn Met Met Asn His Cys Asn Leu Trp Asp Ser His His Pro Glu  
420 425 430

Val Pro Gln Arg Ile Leu Arg Ile Met Cys Arg Leu Glu Glu Leu Gly  
435 440 445

Leu Ala Gly Arg Cys Leu Thr Leu Thr Pro Arg Pro Ala Thr Glu Ala  
450 455 460

Glu Leu Leu Thr Cys His Ser Ala Glu Tyr Val Gly His Leu Arg Ala  
465 470 475 480

Thr Glu Lys Met Lys Thr Arg Glu Leu His Arg Glu Ser Ser Asn Phe  
485 490 495

Asp Ser Ile Tyr Ile Cys Pro Ser Thr Phe Ala Cys Ala Gln Leu Ala  
500 505 510

Thr Gly Ala Ala Cys Arg Leu Val Glu Ala Val Leu Ser Gly Glu Val  
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515  
 520  
 525  
 Leu Asn Gly Ala Ala Val Val Arg Pro Pro Gly His His Ala Glu Gln  
 530 535 540  
 Asp Ala Ala Cys Gly Phe Cys Phe Phe Asn Ser Val Ala Val Ala Ala  
 545 550 555 560  
 Arg His Ala Gln Thr Ile Ser Gly His Ala Leu Arg Ile Leu Ile Val  
 565 570 575  
 Asp Trp Asp Val His His Gly Asn Gly Thr Gln His Met Phe Glu Asp  
 580 585 590  
 Asp Pro Ser Val Leu Tyr Val Ser Leu His Arg Tyr Asp His Gly Thr  
 595 600 605  
 Phe Phe Pro Met Gly Asp Glu Gly Ala Ser Ser Gln Ile Gly Arg Ala  
 610 615 620  
 Ala Gly Thr Gly Phe Thr Val Asn Val Ala Trp Asn Gly Pro Arg Met  
 625 630 635 640  
 Gly Asp Ala Asp Tyr Leu Ala Ala Trp His Arg Leu Val Leu Pro Ile  
 645 650 655  
 Ala Tyr Glu Phe Asn Pro Glu Leu Val Leu Val Ser Ala Gly Phe Asp  
 660 665 670  
 Ala Ala Arg Gly Asp Pro Leu Gly Gly Cys Gln Val Ser Pro Glu Gly  
 675 680 685  
 Tyr Ala His Leu Thr His Leu Leu Met Gly Leu Ala Ser Gly Arg Ile  
 690 695 700  
 Ile Leu Ile Leu Glu Gly Gly Tyr Asn Leu Thr Ser Ile Ser Glu Ser  
 705 710 715 720  
 Met Ala Ala Cys Thr Arg Ser Leu Leu Gly Asp Pro Pro Pro Leu Leu  
 725 730 735  
 Thr Leu Pro Arg Pro Pro Leu Ser Gly Ala Leu Ala Ser Ile Thr Glu  
 740 745 750  
 Thr Ile Gln Val His Arg Arg Tyr Trp Arg Ser Leu Arg Val Met Lys  
 755 760 765

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Val Glu Asp Arg Glu Gly Pro Gly His His His His His His  
770 775 780

<210> 6  
<211> 2349  
<212> DNA  
<213> Artificial

<220>  
<223> DNA encoding residues 73-845 of HDAC6 with a "GHHHHHH" tag at the C-terminus and a "MP" tag at the N-terminus

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gatgagcagt taaatgaatt ccattgcctc tgggatgaca gcttcccgga aggccctgag 120  
cggctccatg ccatcaagga gcaactgata caggagggcc tcctagatcg ctgcgtgtcc 180  
tttcaggccc ggtttgctga aaaggaagag ctgatgttgg ttcacagcct agaatatatt 240  
gatctgatgg aaacaacca gtacatgaat gagggagaac tccgtgtcct agcagacacc 300  
tacgactcag tttatctgca tccgaactca tactcctgtg cctgcctggc ctcaggctct 360  
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aggcctcctg gacatcacgc ccagcacagt cttatggatg gctattgcat gttcaaccac 480  
gtggctgtgg cagcccgcta tgctcaacag aaacaccgca tccggagggg cttatcgtgta 540  
gattgggatg tgcaccacgg tcaaggaaca cagttcacct tcgaccagga ccccagtgtc 600  
ctctatttct ccatccaccg ctacgagcag ggtaggttct ggccccacct gaaggcctct 660  
aactggtcca ccacaggttt cggccaaggc caaggatata ccatcaatgt gccttggaac 720  
caggtgggga tgcgggatgc tgactacatt gctgctttcc tgcacgtcct gctgccagtc 780  
gccctcgagt tccagcctca gctggtcctg gtggctgtcg gatttgatgc cctgcaaggg 840  
gacccaagg gtgagatggc cgccactccg gcagggttcg cccagctaac ccacctgctc 900  
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gagtcacctg gtgccccctg ccggagtgcc caggcttcag tttcctgtgc tctggaagcc 1080  
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gaggaggaca atgtagagga gagcgaggag gaaggaccct gggagcccc tgtgctccca 1200  
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aatcactgca acttgtggga cagccaccac cctgaggtac cccagcgcac cttgcggatc 1320  
atgtgccgtc tggaggagct gggccttgcc gggcgctgcc tcaccctgac accgcgccct 1380  
gccacagagg ctgagctgct cacctgtcac agtgctgagt acgtgggtca tctccgggcc 1440  
acagagaaaa tgaaaaccgc ggagctgcac cgtgagagtt ccaactttga ctccatctat 1500

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atctgcccc a gtaccttcgc ctgtgcacag cttgccactg gcgctgcctg ccgcctggtg 1560  
gaggctgtgc tctcaggaga ggttctgaat ggtgctgctg tgggtgcgtcc cccaggacac 1620  
cacgcagagc aggatgcagc ttgcggtttt tgctttttca actctgtggc tgtggctgct 1680  
cgccatgccc agactatcag tgggcatgcc ctacggatcc tgattgtgga ttgggatgtc 1740  
caccacggta atggaactca gcacatgttt gaggatgacc ccagtgtgct atatgtgtcc 1800  
ctgcaccgct atgatcatgg caccttcttc cccatggggg atgaggggtgc cagcagccag 1860  
atcggccggg ctgcgggcac aggccttcacc gtcaacgtgg catggaacgg gccccgcatg 1920  
ggtgatgctg actacctagc tgcctggcat cgctggtgc ttcccattgc ctacgagttt 1980  
aaccagaac tgggtgctggt ctacagctggc tttgatgctg cacgggggga tccgctgggg 2040  
ggctgccagg tgtcacctga gggttatgcc cacctcacc acctgctgat gggccttgcc 2100  
agtggccgca ttatccttat cctagagggg ggctataacc tgacatccat ctacagagtc 2160  
atggctgcct gcactcgctc cctccttgga gaccaccac ccctgctgac cctgccacgg 2220  
ccccactat caggggccct ggcctcaatc actgagacca tccaagtcca tcgcagatac 2280  
tggcgcagct tacgggtcat gaaggtagaa gacagagaag gaccgggca tcaccatcac 2340  
catcactaa 2349

<210> 7  
<211> 385  
<212> PRT  
<213> Artificial

<220>  
<223> Residues 1-377 of HDAC8 with a "MHHHHHP" tag at the N-terminus  
<400> 7

Met His His His His His His Pro Met Glu Glu Pro Glu Glu Pro Ala  
1 5 10 15

Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr Ser Pro Glu Tyr  
20 25 30

Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys Arg Ala Ser Met  
35 40 45

Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys Gln Met Arg Ile  
50 55 60

Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala Ala Phe His Thr  
65 70 75 80

Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln Glu Gly Asp Asp  
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85

90

95

Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr Asp Cys Pro Ala  
100 105 110

Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly Gly Ala Thr Ile  
115 120 125

Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys Val Ala Ile Asn  
130 135 140

Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu Ala Ser Gly Phe  
145 150 155 160

Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg Leu Arg Arg Lys  
165 170 175

Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His His Gly Asp Gly  
180 185 190

Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met Thr Val Ser Leu  
195 200 205

His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly Asp Val Ser Asp  
210 215 220

Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn Val Pro Ile Gln  
225 230 235 240

Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys Glu Ser Val Leu  
245 250 255

Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val Val Leu Gln Leu  
260 265 270

Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser Phe Asn Met Thr  
275 280 285

Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu Gln Trp Gln Leu  
290 295 300

Ala Thr Leu Ile Leu Gly Gly Gly Gly Tyr Asn Leu Ala Asn Thr Ala  
305 310 315 320

Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly Lys Thr Leu Ser  
325 330 335

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Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr Gly Pro Asp Tyr  
340 345 350

Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg Asn Glu Pro His  
355 360 365

Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn Leu Lys His Val  
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Val  
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SYR-HDAC-5005-C2 sub seq list 2.ST25

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1158